Predictions and Interpretation for Random Effects Models

STAT 245

Our RE model for whale dive duration and sonar

```
rem4 <- glmmTMB(DurAvg ~ DepthAvg + TransClass +
                  SonarA + (1|TagID/TagDayPeriod),
             data = zc_dives,
             REML = FALSE)
```

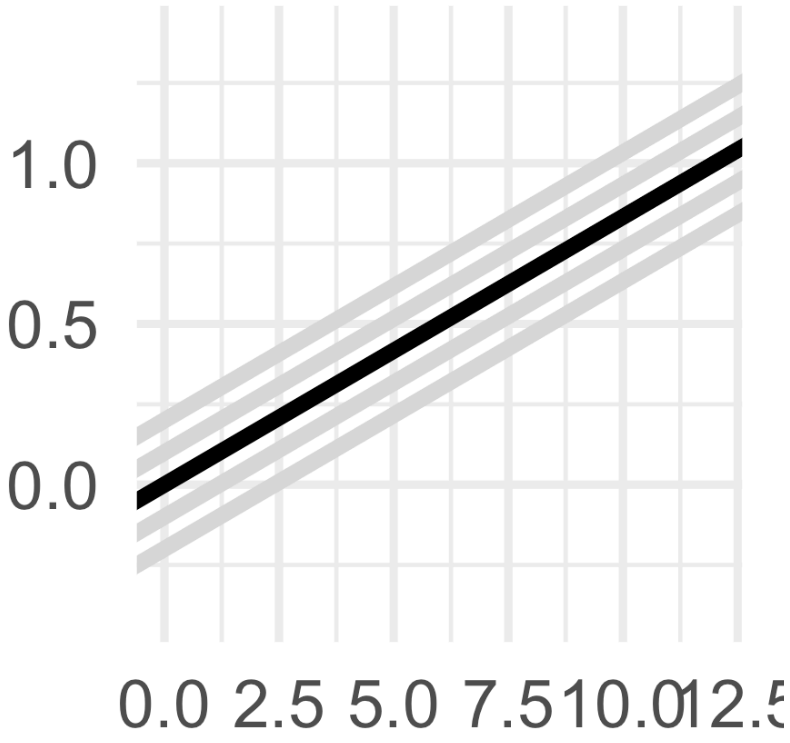
```
summary(rem4)
```

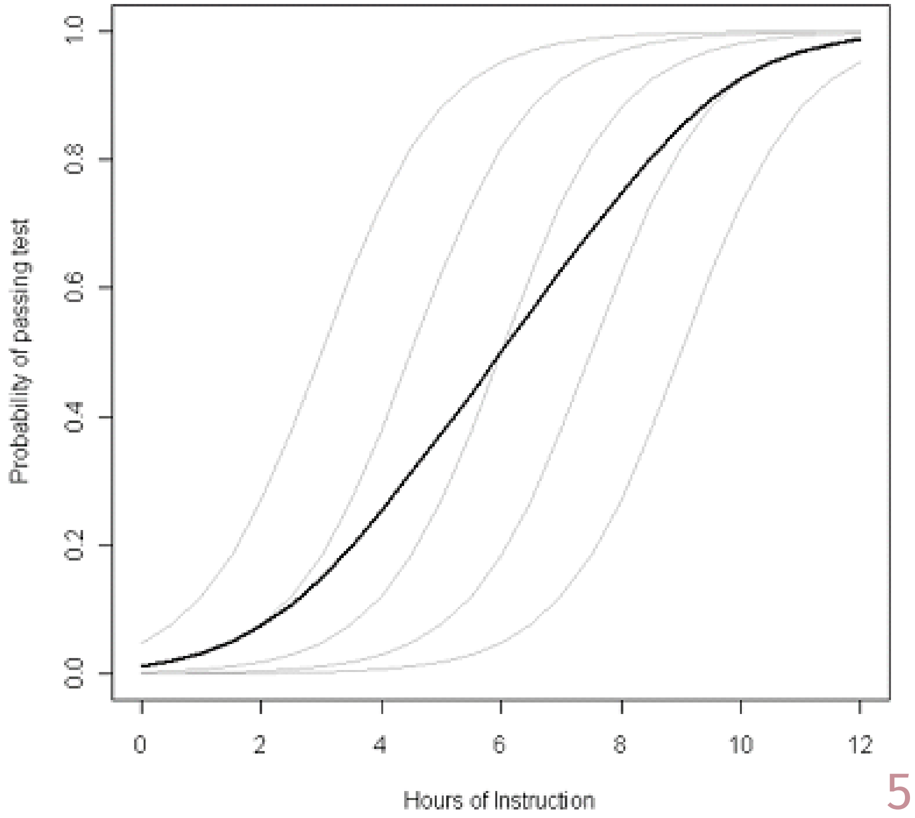
```
##  Family: gaussian  ( identity )
## Formula:
## DurAvg ~ DepthAvg + TransClass + SonarA + (1 | TagID/TagDayPeriod)
## Data: zc_dives
##
##      AIC      BIC   logLik deviance df.resid
##  36240.5  36301.1 -18111.3  36222.5     6174
##
## Random effects:
##
## Conditional model:
##  Groups             Name        Variance Std.Dev.
##  TagDayPeriod:TagID (Intercept)  9.33    3.055
##  TagID              (Intercept)  3.28    1.811
##  Residual                       14.35    3.789
## Number of obs: 6183, groups:  TagDayPeriod:TagID, 2143; TagID, 15
##
## Dispersion estimate for gaussian family (sigma^2): 14.4
##
## Conditional model:
##                    Estimate Std. Error z value Pr(>|z|)
## (Intercept)      10.6143686  0.5522635   19.22  < 2e-16 ***
## DepthAvg          0.0399694  0.0005071   78.83  < 2e-16 ***
## TransClassDay    -0.1605063  0.2540850   -0.63 0.527581
## TransClassDusk   -1.2486613  0.3384696   -3.69 0.000225 ***
## TransClassNight  -2.3023830  0.2554556   -9.01  < 2e-16 ***
## SonarA1           2.8549470  0.6902208    4.14 3.53e-05 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Typical (average) RE Group vs. Population Average

- Random effects models provide predictions for the *average or typical RE group*.
- **For a linear regression model (or any model with the identity link function, that is, no link function), the predicted values for the population average and typical-RE-group average are the same.**
- But with a link function in the mix, **it's different**.

Typical (average) RE Group vs. Population Average





Predictions with CIs for *Typical (average) RE Group*

Easily done, but *do not* include random effects variability

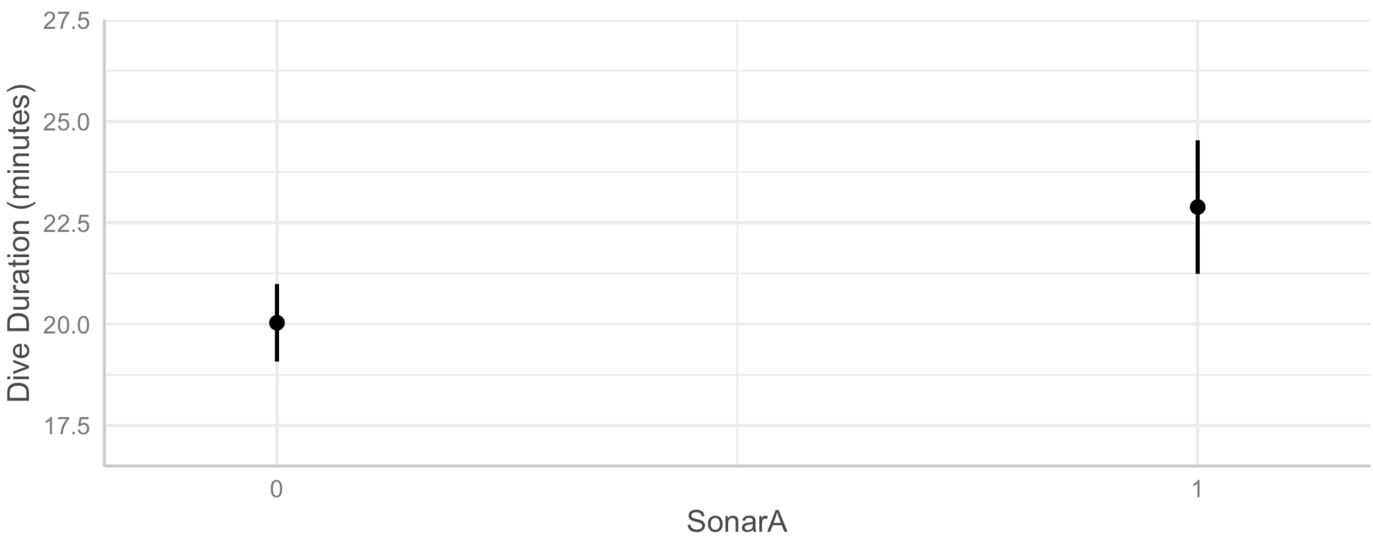
$$y = \beta_0 + \beta_1 x_1 + \ldots \beta_k x_k + \epsilon_{RE} + \epsilon_{resid},$$

$$\epsilon_{RE} \sim N(0, \sigma_{RE}); \epsilon_{resid} \sim N(0, \sigma_{resid})$$

Pred. plot w/ `ggpredict()`

```r
library(ggeffects)
ggpredict(rem4,
          terms = 'SonarA',
          type = 'fixed') |>
  plot() |>
  gf_labs(y = 'Dive Duration (minutes)',
          title = '') |>
  gf_lims(y = c(17, 27))
```

Pred. plot w/ `ggeffects::ggpredict()`



BUT: What uncertainty is included here? Is ϵ_{RE} *included?*

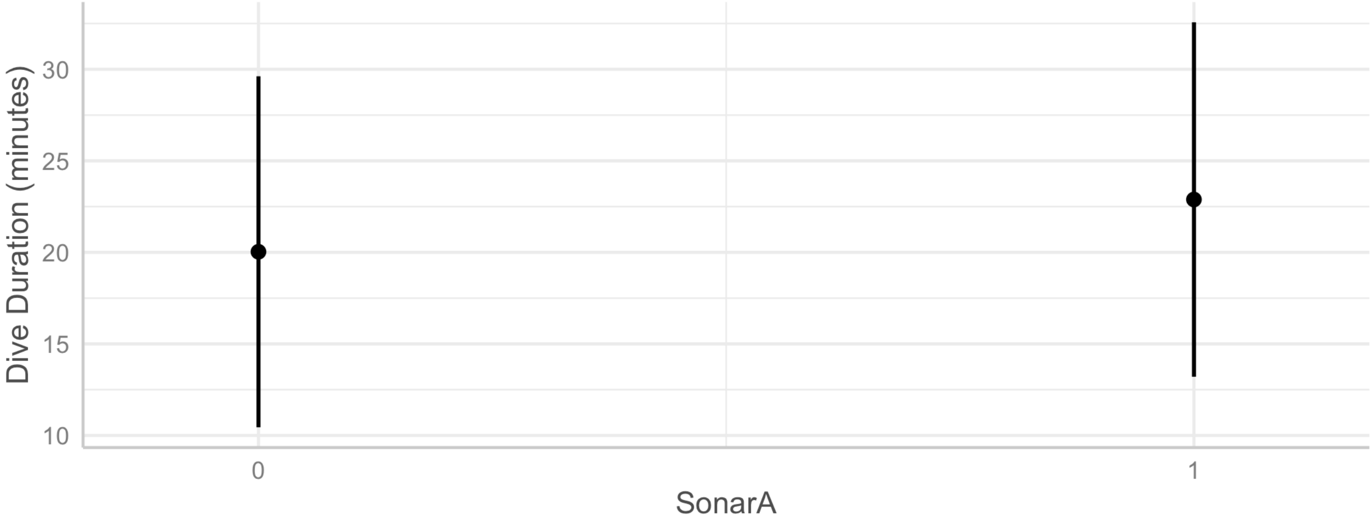
Including ϵ_{RE}

Should you do this? Depends if want to include variation across RE groups (whale/hours)

```r
ggpredict(rem4,
          terms = 'SonarA',
          type = 're') |>
  plot() |>
  gf_labs(y = 'Dive Duration (minutes)',
          title = '')
```

Including ϵ_{RE}

Should you do this? Depends if want to include variation across RE groups (whale/hours)



Parametric bootstrap to the rescue!

How can we get *population average* predictions?

- simulate data, based on our model, for (simulated) new RE groups. (Include uncertainty related to random effects, AND intercept/slope estimates)
- re-fit the model to the simulated data
- make predictions from the re-fitted-to-simulated-data model
- repeat LOTS of times to get a *distribution* of predicted values
- take a point-wise average over all those RE groups (and also use them to find a CI)
- result: population average predictions and confidence intervals.

Parametric Bootstrap

To obtain population-average predictions with CIs

We can do this with help from the function `bootMer()` from the `lme4` package.

Parametric Bootstrap

1. create function that makes predictions from our model.

```
predict_rem4 <- function(model){
  new_dat <- data_grid(
    model,
    terms = 'SonarA',
    condition = c(TagID = "14",
                  TagDayPeriod = "2011-01-06.(18,20]")
  )
  return(predict(model,
                 newdata = new_dat,
                 type = "response",
                 allow.new.levels = TRUE))
}
```

Parametric Bootstrap

2. Simulate, make predictions for many new fake individuals

```r
library(lme4)
# this will take a while
boot_rem4 <- bootMer(rem4,
                     FUN = predict_rem4,
                     nsim = 1000,
                     type = "parametric",
                     use.u = FALSE)
```

Simulation Results

```r
glimpse(boot_rem4$t)
```

```
##  num [1:1000, 1:2] 20.1 19.5 13.6 21.3 18.2 ...
```

```r
# show the first few rows of results
head(boot_rem4$t)
```

```
##          [,1]     [,2]
## [1,] 20.12762 22.54999
## [2,] 19.48603 22.91929
## [3,] 13.56932 16.81862
```

Parametric Bootstrap

3. Compute CIs from simulated-individual predictions

```r
new_data_pboot <- data_grid(rem4,
                       terms = 'SonarA') |>
  mutate(pred = apply(boot_rem4$t, 2, mean),
         CIlow = apply(boot_rem4$t, 2,
                       quantile, probs = 0.025),
         CIhigh = apply(boot_rem4$t, 2,
                        quantile, probs = 0.975)
         )
```

Parametric Bootstrap

3. Compute CIs from simulated-individual predictions

```
glimpse(new_data_pboot)
```

```
## Rows: 2
## Columns: 8
## $ SonarA       <fct> 0, 1
## $ DepthAvg     <dbl> 293.2208, 293.2208
## $ TransClass   <fct> Night, Night
## $ TagDayPeriod <lgl> NA, NA
## $ TagID        <lgl> NA, NA
## $ pred         <dbl> 19.98236, 22.82337
## $ CIlow        <dbl> 14.66732, 17.41859
## $ CIhigh       <dbl> 24.74450, 27.62773
```

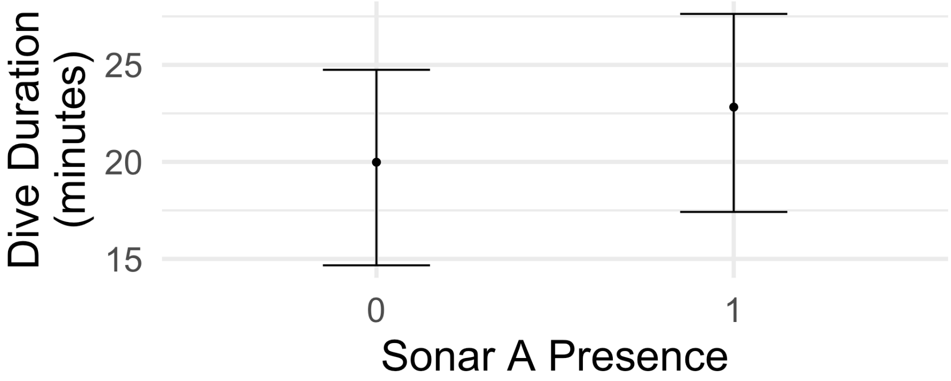
Parametric Bootstrap

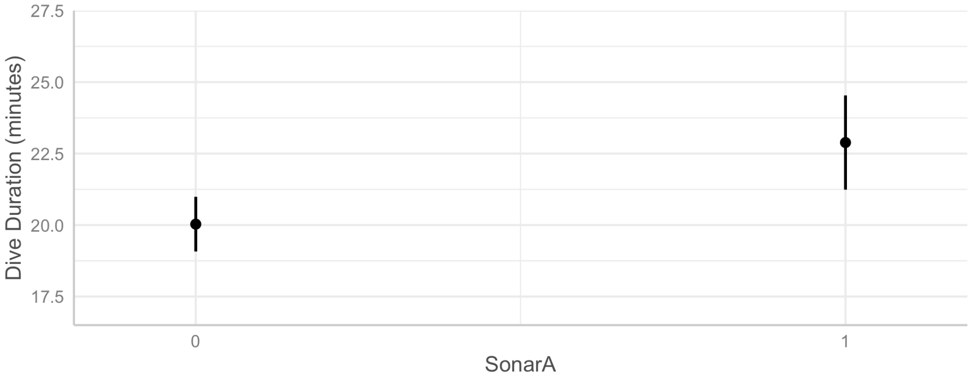
4. Plot results

```r
gf_point(pred ~ SonarA, data = new_data_pboot) |>
  gf_labs(x='Sonar A Presence',
          y='Dive Duration\n(minutes)') |>
  gf_errorbar(CIlow + CIhigh ~ SonarA,
              data = new_data_pboot, width=0.3)
```

Parametric Bootstrap

4. Plot results (& compare w/ ave. RE group)


Dive Duration (minutes)
Sonar A Presence


Dive Duration (minutes)
SonarA